PATENT
Attorney Docket No.: ISIS – 10467
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IN THE CLAIMS

1-13. (cancelled)

14. (currently amended) A method of determining the genotype of a bioagent comprising the steps of:

selecting at least one pair of oligonucleotide primers, wherein one member of said pair of primers hybridizes to a first conserved region of nucleic acid encoding a ribosomal RNA and the other member of said pair of primers hybridizes to a second conserved region of nucleic acid encoding said ribosomal RNA wherein said first and second conserved regions flank a variable nucleic acid region that when amplified creates a unique base composition signature ~~which varies in base composition among~~ at least eight bioagents;

amplifying nucleic acid from at least one said bioagent with said pair of oligonucleotide primers to produce an amplification product;

determining the molecular mass of said amplification product by mass spectrometry;

calculating the base composition of said amplification product from said molecular mass;

comparing said base composition of at least one said bioagent to nineteen ~~eight~~ or more calculated or measured base compositions of amplification products of known bioagents produced by using said at least one pair of oligonucleotide primers, thereby identifying said unknown bioagent at the species level; and

identifying a sub-species characteristic of said bioagent, thereby determining the genotype of said bioagent.

15. (previously presented) The method of claim 14 wherein said sub-species characteristic comprises at least one single nucleotide polymorphism.

16.-28. (cancelled)

29. (previously presented) The method of claim 14 wherein the molecular

masses of said amplification products are determined by ESI-TOF mass spectrometry.

30. (previously presented) The method of claim 14 wherein said bioagent is a bacterium, mold, fungus or parasite.

31. (currently amended) A method of determining the genotype of a bioagent comprising the steps of:

selecting at least one pair of oligonucleotide primers, wherein one member of said pair of primers hybridizes to a first conserved region of a nucleic acid encoding a protein that participates in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, uptake, secretion, antibiotic resistance, virulence, or pathogenicity, and the other member of said pair of primers hybridizes to a second conserved region of said nucleic acid encoding a protein that participates in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, uptake, secretion, antibiotic resistance, virulence, or pathogenicity, wherein said first and second conserved regions flank a variable nucleic acid region that when amplified creates unique base composition signatures ~~which varies~~ among at least eight bioagents;

amplifying nucleic acid from at least one said bioagent with said pair of oligonucleotide primers to produce an amplification product;

determining the molecular mass of said amplification product by mass spectrometry;

calculating the base composition of said amplification product from said molecular mass;

comparing said base composition of at least one said bioagent to nineteen ~~eight~~ or more calculated or measured base compositions of amplification products of known bioagents produced by using said at least one pair of oligonucleotide primers, thereby identifying said unknown bioagent at the species level; and

identifying a sub-species characteristic of said bioagent, thereby determining the genotype of said bioagent.

32. (previously presented) The method of claim 31 wherein said sub-species characteristic comprises at least one single nucleotide polymorphism.

33. (cancelled)

34. (previously presented) The method of claim 31 wherein said sub-species characteristic comprises a pathogenicity factor.

35. (previously presented) The method of claim 34 wherein said pathogenicity factor is a pathogenicity island, a virulence marker, or a toxin gene.

36. (previously presented) The method of claim 35 wherein said toxin gene has been inserted by genetic engineering.

37. (previously presented) The method of claim 31 wherein said molecular masses of said amplification products are determined by ESI-TOF mass spectrometry.

38. (previously presented) The method of claim 31 wherein said bioagent is a bacterium, virus, mold, fungus or parasite.